

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rhode, Peter R.
Jiao, Jin-An
Burkhardt, Martin
Wong, Hing
- (ii) TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 124
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dade International, Inc.
 - (B) STREET: 1717 Deerfield Road
 - (C) CITY: Deerfield
 - (D) STATE: Illinois
 - (E) COUNTRY: USA
 - (F) ZIP: 60015
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US95/09816
 - (B) FILING DATE: 31-JUL-1995
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 - (A) APPLICATION NUMBER: US 08/382,454
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- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/283,302
 - (B) FILING DATE: 29-JUL-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Pearson, Louise S.
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 - (C) REFERENCE/DOCKET NUMBER: STR-4665-CIP2
- (ix) TELECOMMUNICATION INFORMATION:
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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

CCACCATG

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

2

Ser Ile Ser Gln Ala Val His Ala Ala Arg Ala Glu Ile Asn Glu Ala
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Ile Ser Gln Ala Val His Ala Ala His Tyr Glu Ile Asn Glu Ala
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Leu Cys Asn Ile Pro Cys Ser Ala Leu Leu Ser Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Ile Ser Val Gln Pro Ala Phe Ser Val Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Tyr Gly Ser Leu Pro Gln Lys Ser Gln His Gly Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

His Ser Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe
 1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Ser Gln Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGAAGAAT TCGAGCTCGG CCCCCAG

27

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATGATATCA GAGAGAAATA CATACTAACA CAC

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGAAGAAAG AGACTTCGGC CGCTACTTAC

30

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTGTGTTAGT ATGTATTTCT CTCTGATATC TTCAGCTTCC AGCAGTG

47

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCTTCTAGAA GACCACGCTA C

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATGATATCC GGCCGAAGTC TCTTTCTTCC GTTGTC

36

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGGGTTATC AACACCCTGA AAAC

24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTCACAGTTA TCCACTCTGT C

21

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGTCTCCTC AGGTACGGCC GGCCTCTCCA GGTCTTCG

38

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACAGTTATC CACTCTGTCT TTGATATCAC AGGTGTCCT

39

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

His	Ser	Leu	Gly	Lys	Tyr	Leu	Gly	His	Pro	Asp	Lys	Phe
1				5					10			

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

His	Ser	Leu	Gly	Lys	Leu	Leu	Gly	His	Pro	Asp	Lys	Phe
1				5					10			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Arg Gly
1 5 10 15
Arg

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Leu Cys Asn Ile Pro Ser Cys Ala Leu Leu Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGGGGGGCCA TGGCCGAAGA CGACATTGAG GCCGAC 36

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGCGACTA GTCCAGTGTT TCAGAACCGG CTC 33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCCGATA TCTCAGCTTC CAGCAGTGGA GACGACATTG AG

42

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCCCCC GGC CGTACTTAC GTTTCAGTG TTTCAGAACC GG

42

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGGGGCCA TGGCCGAAA CTCCGAAAGG CATTTTCG

37

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGCGACTA GTCCACTCCA CAGTGATGGG GC

32

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

CCCCCCCCGGC CGTACCTGAG GACCACTCCA CAGTGATGG

39

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCCCGATA TCACAGGTGT CTTAAGTGCT AGCGGAGGGG GCGGAAGCGG CGGAGGGGGA

60

AACTCCGAAA GGCATTTTC

78

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGCTTGATAT CACAGGTGTC TTAAGTGGAG

30

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTAGCTCCAC TTAAGACACC TGTGATATCA

30

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCCGGAGGCG GCGGAGACTC CGAAAGGCAT TTCG

34

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGATCGCTAG CGGCGGTGGT GGTTCGGTG GCGGCGGAG

39

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCCCCAGGC TTCCCGGGCC ACCATGCCGT GCAGCAGAGC TC

42

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCCCCGAGC TCGAATTCTC ATAAAGGCC TGGGTGTCTG

40

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCCCAAGC TTCCCGGGCC ACCATGGCTC TGCAGATCCC CAGC

44

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCCCACTT AAGGTCCTTG GGCTGCTCAG CACC

34

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCCCCCCCAT CACTGTGGAG TGGAGGG

27

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCCGAGC TCGAATTCTC ACTGCAGGAG CCCTGCTGG

39

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGGGAAGC TTATGATCAA AGAAGAACAT GTGATCATC

39

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGGCGGGAT CCGTTCTCTG TAGTCTCTGG GAGAGG

36

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGGGGAAGC TTATGGGGGA CACCCGACCA CGTTTCTTGT GGCAGC

46

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGGGGGCCA TGGCCATCAA AGAAGAACAT GTGATCATC

39

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGCGACTA GTGTTCTCTG TAGTCTCTGG GAGAGG

36

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGGGGAAGC TTGATATCTC AGCTTCCAGC AGTAGTATCA AAGAAGAACA TGTGATC 57

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGGGGCGGC CGCTACTTAC GTTTCTCTGG GAGAGGGCTT GGAGC 45

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCGGCGGGAT CCCTTGCTCT GTGCAGATTC AGACC 35

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGGGGGGCCA TGGCCGGATC CGCTAGCGGG GACACCCGAC CACGTTTCTT G 51

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCGGCGACTA GTCTTGCTCT GTGCAGATTC AGACCG

36

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTGTCTTAA GTGGAGCTAG CGGAGGGGGC GGGTCCGGAG GTGGTGGGGA CACCCG

56

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GAAATGACAT TCAAACCTCA GCTGCCACAA GAAACGTGGT CGGGTGTCCC CACCACC

57

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGGGCGGC CGTACCTGAG GACTTGCTCT GTGCAGATTC AG

42

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTAAGTATCT CTCAGGCTGT TCACGCTGCT CACGCTGAAA TCAACGAAGC TGGTCGTG 58

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTAGCACGAC CAGCTTCGTT GATTTTCAGCC TGAGCAGCGT GAACAGCCTG AGAGATAC 58

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTAAGTATCT CTCAGGCTGT TCACGCTGCT CGGGCTGAAA TCAACGAAGC TGGTCGTG 58

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTAGCACGAC CAGCTTCGTT GATTTTCAGCC CGAGCAGCGT GAACAGCCTG AGAGATAC 58

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TTAAGTATCT CTCAGGCTGT TCACGCTGCT CACTACGAAA TCAACGAAGC TGGTCGTG 58

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTAGCAGAC CAGCTTCGTT GATTTTCATAG TGAGCAGCGT GAACAGCCTG AGAGATAC 58

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TTAAGTAACC TGTGCAACAT CCCCTGCAGC GCCCTGCTGA GCTCCG 46

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTAGCGGAGC TCAGCAGGGC GCTGCAGGGG ATGTTGCACA GGTTAC 46

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTAAGTCAGA TCAGCGTGCA GCCCGCCTTC AGCGTGCAGG

40

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTAGCCTGCA CGCTGAAGGC GGGCTGAACG CTGATCTGAC

40

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TTAAGTCCCA AGTACGTGAA GCAGAACACC CTGAAGCTGG CCACCG

46

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTAGCGGTGG CCAGCTTCAG GGTGTTCTGC TTCACGTACT TGGGAC

46

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TTAAGTCACT ATGGCTCCCT GCCGCAGAAG TCCCAGCACG GGCGCG

46

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTAGCGCGCC CGTGCTGGGA CTTCTGCGGC AGGGAGCCAT AGTGAC

46

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTACATCACT CCCTGGGCAA GTGGCTGGGC CACCCGGACA AGTTCG

46

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTAGCGAACT TGTTCGGGTG GCCCAGCCAC TTGCCAGGG AGTGAC

46

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TTAAGTATGG CATCCCAGAA GCGCCCGTCC CAGCGCTCCA AGTACCTGG

49

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTAGCCAGGT ACTTGGAGCG CTGGGACGGG CGCTTCTGGG ATGCCATAC

49

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GATATCTCAG CTTCCAGCAG TGAAGACGAC ATTGAGGCCG ACCAC

45

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCGGTTCTGA AACACTGGAA ACGTAAGTAG CGGCCG

36

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser	Ser	Ser	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His
1				5					10	

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

Pro Val Leu Lys His Trp Lys Arg
1 5

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

GATATCACAG GTGTCTTAAG TGGAGCTAGC GGAGGGGGCG GAAGCGGCGG AGGGGGAAAC 60
TCCGAAAGGC AT 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

ATCACTGTGG AGTGGTCCTC AGGTACGGCC GCC 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Val Leu Ser Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn

1

5

10

15

Ser Glu Arg His
20

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ile Thr Val Glu Trp Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GATATCTCAG CTTCCAGCAG TGAAGACGAC ATTGAGGCCG ACCAC

45

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCGGTTCTGA AACACTGGAA ACGTAAGTAG CGGCCG

36

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ser Ser Ser Glu Asp Asp Ile Glu Ala Asp His
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Pro Val Leu Lys His Trp Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATATCACAG GTGTCTTAAG TGGAGCTAGC GCGGGTGGTG GTTCCGGTGG CGGCGGAGAC 60
TCCGAAAGGC AT 72

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATCACTGTGG AGTGGTCCTC AGGTACGGCC GCC 33

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Val Leu Ser Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp
1 5 10 15

Ser Glu Arg His
 20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ile Thr Val Glu Trp Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GATATCTCAG CTTCCAGCAG TATCAAAGAA GAACATGTGA TCATC

45

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CCAGAGACTA CAGAGAACAA ACGTAAGTAG CGGCCG

36

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Ser Ser Ile Lys Glu Glu His Val Ile Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Pro Glu Thr Thr Glu Asn Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GATATCACAG GTGTCTTAAG TGGAGCTAGC GGAGGGGGCG GGTTCGGAGG TGGTGGGGAC 60
ACCCGACCAC GTTTCTTGTG GCAGCTGAAG 90

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCTGAATCTG CACAGAGCAA GTCCTCAGGT ACGGCCG 37

(2) INFORMATION FOR SEQ ID NO:97:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Thr Arg Pro Arg Phe Leu Trp Gln Leu Lys
20 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

14

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGTATGTAAA AATAAACATC ACAG

24

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCTTTGCTTA CGGAGTTACT C

21

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCCGGGCCAC CATGCCGTGC AGCAGAGCTC TGATTCTGGG GGTCCTCGCC CTGAACACCA

60

TGCTCAGCCT CTGCGGAGGT GAAGACGACA TTGAG

95

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGATCAGGTG GCACCTCCAG ACACCCAGGG CCTTTATGAG AATTC

45

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
1           5           10           15

Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu
          20           25
```

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```
Arg Ser Gly Gly Thr Ser Arg His Pro Gly Pro Leu
1           5           10
```

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
AAGCTTCCCG GGCCACCATG GCTCTGCAGA TCCCCAGCCT CTCCTCTCA GCTGCTGTGG      60
TGGTGCTGAT GGTGCTGAGC AGCCCAAGGA CCTTAAGTAT CTCTCAGGCT GTTCACGCTG      120
CTCACGCTGA AATCAACGAA GCTGGTCGTG CTAGCGGAGG GGGCGGAAGC GGCGGAGGGG      180
GAAACTCCGA AAGG                                     194
```

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CCTCCTCCAG CAGGGCTCCT GCAGTGAGAA TTCGAGCTC

39

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ala	Leu	Gln	Ile	Pro	Ser	Leu	Leu	Leu	Ser	Ala	Ala	Val	Val	Val
1				5					10					15	
Leu	Met	Val	Leu	Ser	Ser	Pro	Arg	Thr	Leu	Ser	Ile	Ser	Gln	Ala	Val
			20					25					30		
His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly	Arg	Ala	Ser	Gly	Gly
			35				40					45			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Asn	Ser	Glu	Arg					
			50				55								

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Pro	Pro	Pro	Ala	Gly	Leu	Leu	Gln
1					5		

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CCCCCCCCGC GGCCGCCCA CCATGGGACT GAGTAACATT CTC

43

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCCCCGCGG CCGCTTTAAA AACATGTATC ACTTTT

36

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCGCCA TGGCCGCTAG CGGAGGGGGC GGAAGC

36

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CCCGGGGCCT CGAGTGAAGA CGACATTGAG GCCGAC

36

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CCCCCACTA GTCCACTCCA CAGTGATGGG GCT

33

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CCCCCCCCCG GGACCAGTGT TTCAGAACCG GCTCCTC

37

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TCGAGGAACC GCCACCGCCA GAACCGCCGC CACCGGAACC ACCACCGCCG CTGCCACCGC

60

CACCA

65

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTAGTGGTGG CGGTGGCAGC GCGGTGGTG GTTCCGGTGG CCGCGGTTCT GGCGGTGGCG

60

GTTCC

65

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTTGGAATC TTGACTAAGA GG

22

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

CAGGTCGAAT TCTCATTCCA TCGGCATGTA CTCTTCTTCC TCCCAGTGTT TCAGAACCGG

60

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..1382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val
1 5 10

47

GTG	GTG	CTG	ATG	GTG	CTG	AGC	AGC	CCA	AGG	ACC	TTA	AGT	ATC	TCT	CAG	95
Val	Val	Leu	Met	Val	Leu	Ser	Ser	Pro	Arg	Thr	Leu	Ser	Ile	Ser	Gln	
15					20					25					30	
GCT	GTT	CAC	GCT	GCT	CAC	GCT	GAA	ATC	AAC	GAA	GCT	GGT	CGT	GCT	AGC	143
Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly	Arg	Ala	Ser	
				35					40					45		
GGA	GGG	GGC	GGA	AGC	GGC	GGA	GGG	GGA	AAC	TCC	GAA	AGG	CAT	TTC	GTG	191
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Asn	Ser	Glu	Arg	His	Phe	Val	
			50					55					60			
GTC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	TAC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	239
Val	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Tyr	Thr	Asn	Gly	Thr	Gln	Arg	Ile	
		65					70					75				
CGG	CTC	GTG	ACC	AGA	TAC	ATC	TAC	AAC	CGG	GAG	GAG	TAC	GTG	CGC	TAC	287
Arg	Leu	Val	Thr	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Val	Arg	Tyr	
	80					85					90					
GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	GCG	GTG	ACC	GAG	CTG	GGG	CGG	CCA	335
Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	
95					100					105					110	
GAC	GCC	GAG	TAC	TGG	AAC	AGC	CAG	CCG	GAG	ATC	CTG	GAG	CGA	ACG	CGG	383
Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Pro	Glu	Ile	Leu	Glu	Arg	Thr	Arg	
				115					120					125		
GCC	GAG	GTG	GAC	ACG	GCG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	CCG	GAG	ACC	431
Ala	Glu	Val	Asp	Thr	Ala	Cys	Arg	His	Asn	Tyr	Glu	Gly	Pro	Glu	Thr	
			130					135					140			
AGC	ACC	TCC	CTG	CGG	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC	CTG	479
Ser	Thr	Ser	Leu	Arg	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	
		145					150					155				
TCC	AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG	GTG	527
Ser	Arg	Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	
	160					165					170					
ACA	GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT	GGC	575
Thr	Asp	Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	
175					180					185					190	
CAG	GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	623
Gln	Glu	Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	
				195					200					205		
GAC	TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	671
Asp	Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	
			210					215					220			
GGA	GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	719
Gly	Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	

225					230					235						
ATC Ile	ACT Thr 240	GTG Val	GAG Glu	TGG Trp	ACT Thr	AGT Ser 245	GGT Gly	GGC Gly	GGT Gly	GGC Gly	AGC Ser 250	GGC Gly	GGT Gly	GGT Gly	GGT Gly	767
TCC Ser 255	GGT Gly	GGC Gly	GGC Gly	GGT Gly	TCT Ser 260	GGC Gly	GGT Gly	GGC Gly	GGT Gly	TCC Ser 265	TCG Ser	AGT Ser	GAA Glu	GAC Asp	GAC Asp 270	815
ATT Ile	GAG Glu	GCC Ala	GAC Asp	CAC His 275	GTA Val	GGC Gly	TTC Phe	TAT Tyr	GGT Gly 280	ACA Thr	ACT Thr	GTT Val	TAT Tyr	CAG Gln 285	TCT Ser	863
CCT Pro	GGA Gly	GAC Asp	ATT Ile 290	GGC Gly	CAG Gln	TAC Tyr	ACA Thr	CAT His 295	GAA Glu	TTT Phe	GAT Asp	GGT Gly	GAT Asp 300	GAG Glu	TTG Leu	911
TTC Phe	TAT Tyr	GTG Val 305	GAC Asp	TTG Leu	GAT Asp	AAG Lys	AAG Lys 310	AAA Lys	ACT Thr	GTC Val	TGG Trp	AGG Arg 315	CTT Leu	CCT Pro	GAG Glu	959
TTT Phe 320	GGC Gly	CAA Gln	TTG Leu	ATA Ile	CTC Leu	TTT Phe 325	GAG Glu	CCC Pro	CAA Gln	GGT Gly	GGA Gly 330	CTG Leu	CAA Gln	AAC Asn	ATA Ile	1007
GCT Ala 335	GCA Ala	GAA Glu	AAA Lys	CAC His	AAC Asn 340	TTG Leu	GGA Gly	ATC Ile	TTG Leu	ACT Thr 345	AAG Lys	AGG Arg	TCA Ser	AAT Asn	TTC Phe 350	1055
ACC Thr	CCA Pro	GCT Ala	ACC Thr	AAT Asn 355	GAG Glu	GCT Ala	CCT Pro	CAA Gln	GCG Ala 360	ACT Thr	GTG Val	TTC Phe	CCC Pro	AAG Lys 365	TCC Ser	1103
CCT Pro	GTG Val	CTG Leu	CTG Leu 370	GGT Gly	CAG Gln	CCC Pro	AAC Asn	ACC Thr 375	CTT Leu	ATC Ile	TGC Cys	TTT Phe	GTG Val 380	GAC Asp	AAC Asn	1151
ATC Ile	TTC Phe 385	CCA Pro	CCT Pro	GTG Val	ATC Ile	AAC Asn	ATC Ile 390	ACA Thr	TGG Trp	CTC Leu	AGA Arg	AAT Asn 395	AGC Ser	AAG Lys	TCA Ser	1199
GTC Val	ACA Thr 400	GAC Asp	GGC Gly	GTT Val	TAT Tyr	GAG Glu 405	ACC Thr	AGC Ser	TTC Phe	CTC Leu	GTC Val 410	AAC Asn	CGT Arg	GAC Asp	CAT His	1247
TCC Ser 415	TTC Phe	CAC His	AAG Lys	CTG Leu	TCT Ser 420	TAT Tyr	CTC Leu	ACC Thr	TTC Phe	ATC Ile 425	CCT Pro	TCT Ser	GAT Asp	GAT Asp	GAC Asp 430	1295
ATT Ile	TAT Tyr	GAC Asp	TGC Cys	AAG Lys 435	GTG Val	GAG Glu	CAC His	TGG Trp	GGC Gly 440	CTG Leu	GAG Glu	GAG Glu	CCG Pro	GTT Val 445	CTG Leu	1343

AAA CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG
 Lys His Trp Ser Arg Ala Ser His His His His His His
 450 455

1385

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..1505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG	47
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val	
460 465 470	
GTG GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG	95
Val Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln	
475 480 485	
GCT GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC	143
Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser	
490 495 500 505	
GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG	191
Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val	
510 515 520	
GTC CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA	239
Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile	
525 530 535	
CGG CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC	287
Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr	
540 545 550	
GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA	335
Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro	
555 560 565	
GAC GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG	383
Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg	
570 575 580 585	
GCC GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC	431

Ala	Glu	Val	Asp	Thr	Ala	Cys	Arg	His	Asn	Tyr	Glu	Gly	Pro	Glu	Thr	
				590					595					600		
AGC	ACC	TCC	CTG	CGG	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC	CTG	479
Ser	Thr	Ser	Leu	Arg	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	
			605					610					615			
TCC	AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG	GTG	527
Ser	Arg	Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	
			620					625					630			
ACA	GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT	GGC	575
Thr	Asp	Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	
			635					640					645			
CAG	GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	623
Gln	Glu	Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	
					655					660					665	
GAC	TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	671
Asp	Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	
				670					675						680	
GGA	GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	719
Gly	Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	
			685					690						695		
ATC	ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGT	GGC	AGC	GGC	GGT	GGT	GGT	767
Ile	Thr	Val	Glu	Trp	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
			700					705					710			
TCC	GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	815
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Glu	Asp	Asp	
			715					720					725			
ATT	GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	863
Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	
			730					735					740		745	
CCT	GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	GAT	GAG	TTG	911
Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	
				750					755					760		
TTC	TAT	GTG	GAC	TTG	GAT	AAG	AAG	AAA	ACT	GTC	TGG	AGG	CTT	CCT	GAG	959
Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	
			765					770						775		
TTT	GGC	CAA	TTG	ATA	CTC	TTT	GAG	CCC	CAA	GGT	GGA	CTG	CAA	AAC	ATA	1007
Phe	Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	
			780					785					790			
GCT	GCA	GAA	AAA	CAC	AAC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	TCA	AAT	TTC	1055
Ala	Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	
			795					800					805			

ACC	CCA	GCT	ACC	AAT	GAG	GCT	CCT	CAA	GCG	ACT	GTG	TTC	CCC	AAG	TCC	1103
Thr	Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	
810					815					820					825	
CCT	GTG	CTG	CTG	GGT	CAG	CCC	AAC	ACC	CTT	ATC	TGC	TTT	GTG	GAC	AAC	1151
Pro	Val	Leu	Leu	Gly	Gln	Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	
				830					835					840		
ATC	TTC	CCA	CCT	GTG	ATC	AAC	ATC	ACA	TGG	CTC	AGA	AAT	AGC	AAG	TCA	1199
Ile	Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	
			845					850					855			
GTC	ACA	GAC	GGC	GTT	TAT	GAG	ACC	AGC	TTC	CTC	GTC	AAC	CGT	GAC	CAT	1247
Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	
		860					865					870				
TCC	TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC	ATC	CCT	TCT	GAT	GAT	GAC	1295
Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	
	875					880					885					
ATT	TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	CTG	GAG	GAG	CCG	GTT	CTG	1343
Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	
890					895					900					905	
AAA	CAC	TGG	GAA	CCT	GAG	ATT	CCA	GCC	CCC	ATG	TCA	GAG	CTG	ACA	GAA	1391
Lys	His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	
				910					915					920		
ACT	GTG	GTG	TGT	GCC	CTG	GGG	TTG	TCT	GTG	GGC	CTT	GTG	GGC	ATC	GTG	1439
Thr	Val	Val	Cys	Ala	Leu	Gly	Leu	Ser	Val	Gly	Leu	Val	Gly	Ile	Val	
			925					930					935			
GTG	GGC	ACC	ATC	TTC	ATC	ATT	CAA	GGC	CTG	CGA	TCA	GGT	GGC	ACC	TCC	1487
Val	Gly	Thr	Ile	Phe	Ile	Ile	Gln	Gly	Leu	Arg	Ser	Gly	Gly	Thr	Ser	
		940					945					950				
AGA	CAC	CCA	GGG	CCT	TTA	TGA										1508
Arg	His	Pro	Gly	Pro	Leu											
			955													

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 6..1382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG	47
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val	
505 510	
GTG GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG	95
Val Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln	
515 520 525 530	
GCT GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC	143
Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser	
535 540 545	
GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG	191
Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val	
550 555 560	
GTC CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA	239
Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile	
565 570 575	
CGG CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC	287
Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr	
580 585 590	
GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA	335
Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro	
595 600 605 610	
GAC GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG	383
Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg	
615 620 625	
GCC GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC	431
Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr	
630 635 640	
AGC ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG	479
Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu	
645 650 655	
TCC AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG	527
Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val	
660 665 670	
ACA GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC	575
Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly	
675 680 685 690	
CAG GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG	623
Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly	

695					700					705						
GAC Asp	TGG Trp	ACC Thr	TTC Phe 710	CAG Gln	GTC Val	CTG Leu	GTC Val	ATG Met 715	CTG Leu	GAG Glu	ATG Met	ACC Thr	CCT Pro 720	CAT His	CAG Gln	671
GGA Gly	GAG Glu	GTC Val 725	TAC Tyr	ACC Thr	TGC Cys	CAT His	GTG Val 730	GAG Glu	CAT His	CCC Pro	AGC Ser	CTG Leu 735	AAG Lys	AGC Ser	CCC Pro	719
ATC Ile	ACT Thr 740	GTG Val	GAG Glu	TGG Trp	ACT Thr	AGT Ser 745	GGT Gly	GGC Gly	GGT Gly	GGC Gly	AGC Ser 750	GGC Gly	GGT Gly	GGT Gly	GGT Gly	767
TCC Ser 755	GGT Gly	GGC Gly	GGC Gly	GGT Gly	TCT Ser 760	GGC Gly	GGT Gly	GGC Gly	GGT Gly	TCC Ser 765	TCG Ser	AGT Ser	GAA Glu	GAC Asp	GAC Asp 770	815
ATT Ile	GAG Glu	GCC Ala	GAC Asp 775	CAC His	GTA Val	GGC Gly	TTC Phe	TAT Tyr 780	GGT Gly	ACA Thr	ACT Thr	GTT Val	TAT Tyr 785	CAG Gln	TCT Ser	863
CCT Pro	GGA Gly	GAC Asp	ATT Ile 790	GGC Gly	CAG Gln	TAC Tyr	ACA Thr	CAT His 795	GAA Glu	TTT Phe	GAT Asp	GGT Gly	GAT Asp 800	GAG Glu	TTG Leu	911
TTC Phe	TAT Tyr	GTG Val 805	GAC Asp	TTG Leu	GAT Asp	AAG Lys	AAG Lys 810	AAA Lys	ACT Thr	GTC Val	TGG Trp	AGG Arg 815	CTT Leu	CCT Pro	GAG Glu	959
TTT Phe 820	GGC Gly	CAA Gln	TTG Leu	ATA Ile	CTC Leu	TTT Phe 825	GAG Glu	CCC Pro	CAA Gln	GGT Gly	GGA Gly	CTG Leu 830	CAA Gln	AAC Asn	ATA Ile	1007
GCT Ala 835	GCA Ala	GAA Glu	AAA Lys	CAC His	AAC Asn 840	TTG Leu	GGA Gly	ATC Ile	TTG Leu	ACT Thr 845	AAG Lys	AGG Arg	TCA Ser	AAT Asn	TTC Phe 850	1055
ACC Thr	CCA Pro	GCT Ala	ACC Thr 855	AAT Asn	GAG Glu	GCT Ala	CCT Pro	CAA Gln 860	GCG Ala	ACT Thr	GTG Val	TTC Phe	CCC Pro	AAG Lys 865	TCC Ser	1103
CCT Pro	GTG Val	CTG Leu	CTG Leu 870	GGT Gly	CAG Gln	CCC Pro	AAC Asn	ACC Thr 875	CTT Leu	ATC Ile	TGC Cys	TTT Phe	GTG Val 880	GAC Asp	AAC Asn	1151
ATC Ile	TTC Phe 885	CCA Pro	CCT Pro	GTG Val	ATC Ile	AAC Asn	ATC Ile 890	ACA Thr	TGG Trp	CTC Leu	AGA Arg	AAT Asn 895	AGC Ser	AAG Lys	TCA Ser	1199
GTC Val 900	ACA Thr	GAC Asp	GGC Gly	GTT Val	TAT Tyr	GAG Glu 905	ACC Thr	AGC Ser	TTC Phe	CTC Leu	GTC Val 910	AAC Asn	CGT Arg	GAC Asp	CAT His	1247

TCC	TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC	ATC	CCT	TCT	GAT	GAT	GAC	1295
Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	
915					920					925					930	
ATT	TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	CTG	GAG	GAG	CCG	GTT	CTG	1343
Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	
				935					940					945		
AAA	CAC	TGG	GAG	GAA	GAA	GAG	TAC	ATG	CCG	ATG	GAA	TGA				1382
Lys	His	Trp	Glu	Glu	Glu	Glu	Tyr	Met	Pro	Met	Glu	*				
			950					955								

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Ala	Pro	Tyr	Ser	Thr	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Glu	Thr	Pro
1				5					10					15